



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.

(ii) TITLE OF INVENTION: ANTI-VEGF ANTIBODIES

(iii) NUMBER OF SEQUENCES: 131

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/908,469
(B) FILING DATE: 06-AUG-97
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/833,504
(B) FILING DATE: 07-APR-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Cui, Steven X.
(B) REGISTRATION NUMBER: 44,637
(C) REFERENCE/DOCKET NUMBER: P1093P1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650/225-8674
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Ala Asp Phe
1 5 10 15

Lys Arg

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Tyr Pro His Tyr Tyr Gly Ser Ser His Trp Tyr Phe Asp Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Phe Thr Ser Ser Leu His Ser
1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gln Gln Tyr Ser Thr Val Pro Trp Thr
1 5

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 123 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	1	5	10	15
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	20	25	30	
Asn	Tyr	Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	35	40	45	
Glu	Trp	Val	Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Gly	Glu	Pro	Thr	Tyr	50	55	60	
Ala	Ala	Asp	Phe	Lys	Arg	Arg	Phe	Thr	Phe	Ser	Leu	Asp	Thr	Ser	65	70	75	
Lys	Ser	Thr	Ala	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	80	85	90	
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Tyr	Pro	His	Tyr	Tyr	Gly	Ser	95	100	105	
Ser	His	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	110	115	120	
Val	Ser	Ser																

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	1	5	10	15
Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser	Gln	Asp	Ile	Ser	20	25	30	
Asn	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	35	40	45	
Val	Leu	Ile	Tyr	Phe	Thr	Ser	Ser	Leu	His	Ser	Gly	Val	Pro	Ser	50	55	60	
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	65	70	75	
Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	80	85	90	

Tyr Ser Thr Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
95 100 105
Ile Lys Arg

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Gln Pro Gly
1 5 10 15
Glu Thr Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
20 25 30
Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
35 40 45
Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr
50 55 60
Ala Ala Asp Phe Lys Arg Arg Phe Thr Phe Ser Leu Glu Thr Ser
65 70 75
Ala Ser Thr Ala Tyr Leu Gln Ile Ser Asn Leu Lys Asn Asp Asp
80 85 90
Thr Ala Thr Tyr Phe Cys Ala Lys Tyr Pro His Tyr Tyr Gly Ser
95 100 105
Ser His Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr
110 115 120
Val Ser Ser

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu
1 5 10 15
Gly Asp Arg Val Ile Ile Ser Cys Ser Ala Ser Gln Asp Ile Ser
20 25 30
Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys
35 40 45

Val	Leu	Ile	Tyr	Phe	Thr	Ser	Ser	Leu	His	Ser	Gly	Val	Pro	Ser
				50					55					60
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Ser	Leu	Thr	Ile
				65					70					75
Ser	Asn	Leu	Glu	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln
				80					85					90
Tyr	Ser	Thr	Val	Pro	Trp	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu
				95					100					105
Ile	Lys	Arg												

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly
1				5					10					15
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser
				20					25					30
Ser	Tyr	Ala	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
				35					40					45
Glu	Trp	Val	Ser	Val	Ile	Ser	Gly	Asp	Gly	Gly	Ser	Thr	Tyr	Tyr
				50					55					60
Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser
				65					70					75
Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp
				80					85					90
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Phe	Asp	Tyr	Trp	Gly	Gln
				95					100					105
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser							
				110										

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val
1				5					10					15

Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ser	20	25	30
Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	35	40	45
Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Ser	Leu	Glu	Ser	Gly	Val	Pro	Ser	50	55	60
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	65	70	75
Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	80	85	90
Tyr	Asn	Ser	Leu	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	95	100	105
Ile Lys Arg																	

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	1	5	10	15
Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser	Gln	Asp	Ile	Ser	20	25	30	
Asn	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	35	40	45	
Leu	Leu	Ile	Tyr	Phe	Thr	Ser	Ser	Leu	His	Ser	Gly	Val	Pro	Ser	50	55	60	
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	65	70	75	
Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	80	85	90	
Tyr	Ser	Thr	Val	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	95	100	105	
Ile Lys																		

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	
1				5					10					15	
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	
				20					25					30	
Asn	Tyr	Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
				35					40					45	
Glu	Trp	Val	Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Gly	Glu	Pro	Thr	Tyr	
				50					55					60	
Ala	Ala	Asp	Phe	Lys	Arg	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	
				65					70					75	
Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	
				80					85					90	
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Tyr	Pro	His	Tyr	Tyr	Gly	Ser	
				95					100					105	
Ser	His	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	
				110					115					120	
Val	Ser	Ser													

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	
1				5					10					15	
Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser	Gln	Asp	Ile	Ser	
				20					25					30	
Asn	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	
				35					40					45	
Leu	Leu	Ile	Tyr	Phe	Thr	Ser	Ser	Leu	His	Ser	Gly	Val	Pro	Ser	
				50					55					60	
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	
				65					70					75	
Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	
				80					85					90	
Tyr	Ser	Thr	Val	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	
				95					100					105	
Ile	Lys														

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	
1				5					10					15	
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	
				20					25					30	
Asn	Tyr	Gly	Met	Asn	Trp	Ile	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
				35					40					45	
Glu	Trp	Val	Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Gly	Glu	Pro	Thr	Tyr	
				50					55					60	
Ala	Ala	Asp	Phe	Lys	Arg	Arg	Phe	Thr	Ile	Ser	Leu	Asp	Thr	Ser	
				65					70					75	
Ala	Ser	Thr	Val	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	
				80					85					90	
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Tyr	Pro	His	Tyr	Tyr	Gly	Ser	
				95					100					105	
Ser	His	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	
				110					115					120	
Val	Ser	Ser													

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Pro	Lys	Asn	Ser	Ser	Met	Ile	Ser	Asn	Thr	Pro	
1				5					10		

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

His	Gln	Ser	Leu	Gly	Thr	Gln	
1				5			

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

His Gln Asn Leu Ser Asp Gly Lys
1 5

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

His Gln Asn Ile Ser Asp Gly Lys
1 5

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

Val Ile Ser Ser His Leu Gly Gln
1 5

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

GATTTCAAAC GTCGTNYTAC TWTTTCTAGA GACAACTCCA AAAACACABY 50
TTACCTGCAG ATGAAC 66

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

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GATTTCAAAC GTCGTNYTAC TWTTTCTTTA GACACCTCCG CAAGCACABY 50
TTACCTGCAG ATGAAC 66

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AGCCTGCGCG CTGAGGACAC TGCCGTCTAT TACTGTDYAA RGTACCCCCA 50
CTATTATGGG 60

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CTCAGCGCGC AGGCTGTTCA TCTGCAGGTA 30

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCTGATATCC AGTTGACCCA GTCCCCG 27

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCTGGGACGG ATTACACTCT GACCATC 27

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CGTTTGTCCCT GTGCARYTTC TGGCTATACC TTCACCAACT ATGGTATGAA 50
CTGGRTCCGT CAGGCCCCGG GTAAG 75

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATATCCAGT TGACCCAGTC CCCG 24

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCTCCGAAAG TACTGATTTA C 21

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CGTCGTTTCA CTTTTTCTGC AGACACCTCC AGCAACACAG TATACCTGCA 50
GATG 54

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTATTACTGT GCAAAGTACC CCCAC 25

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGGACGGATT TCACTCTGAC CATC 24

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGTATGAACT GGGTCCGTCA GGCCCC 26

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CGTCGTTTCA CTTTTTCTTT AGACACCTCC AAAAGCACAG CATACTGCA 50

GATGAAC 57

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGGTCACCAT CACCTGCTAA GCATAATAAT AATAAAGCAA CTATTTAAAC 50

TGG 53

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCGCAAGTCA GGATATTTAA TAATAATAAT AATGGTATCA ACAGAAACCA 50
GG 52

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GTCTATTACT GTGCAAAGTA ATAACACTAA TAAGGGAGCA GCCACTGG 48

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GGTACCCCCA CTATTATTAA TAATAATAAT GGTATTTTCGA CGTCTGGGG 49

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CACTATTATG GGAGCAGCCA CTAATAATAA TAAGTCTGGG TCAAGGAACC 50
CTG 53

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs

(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TCCTGTGCAG CTTCTGGCTA ATAATTCTAA TAATAAGGTA TGAAGTGGGT 50
CCG 53

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GAATGGGTTG GATGGATTAA CTAATAATAA GGTAAACCGA CCTATGCTGC 50
GG 52

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTGTGCAAAG TACCCGTAAT ATTAATAATA ATAACACTGG TATTTGAC 49

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CGTTTCACTT TTTCTTAAGA CTAATCCAAA TAAACAGCAT ACCTGCAG 48

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GAATGGGTTG GATGGATTTA ATAATAATAA GGTGAACCGA CCTATG 46

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGGTCACCAT CACCTGCNNS GCANNSNNSN NSNNSAGCAA CTATTTAAAC 50

TGG 53

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GCGCAAGTCA GGATATTNNS NNSNNSNNSN NSTGGTATCA ACAGAAACCA 50

GG 52

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GTCTATTACT GTGCAAAGNN SNNSCACNNS NNSGGGAGCA GCCACTGG 48

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGTACCCCCA CTATTATNNS NNSNNSNNSN GGTATTTTCA CGTCTGGGG 49

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CACTATTATG GGAGCAGCCA CNNSNNSNNS NNSGTCTGGG GTCAAGGAAC 50
CCTG 54

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TCCTGTGCAG CTTCTGGC NN SNNSTTCNNS NNSNNSGGTA TGAAGTGGGT 50
CCG 53

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GAATGGGTTG GATGGATTAA CNNSNNSNNS GGTNNSCCGA CCTATGCTGC 50
GG 52

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CTGTGCAAAG TACCCGNNST ATNNSNNSNN SNNSCACTGG TATTTGAC 49
1

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs

(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CGTTTCACTT TTTCTNNSGA CNNSTCCAAA NNSACAGCAT ACCTGCAG 48

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GAATGGGTTG GATGGATTNN SNNSNNSNNS GGTGAACCGA CCTATG 46

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Tyr Pro Tyr Tyr Arg Gly Thr Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Tyr Pro Tyr Tyr Ile Asn Lys Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Tyr Pro Tyr Tyr Tyr Gly Thr Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Tyr Pro Tyr Tyr Tyr Asn Gln Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Tyr Pro Tyr Tyr Ile Ala Lys Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Tyr Pro Tyr Tyr Arg Asp Asn Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Tyr Pro Tyr Tyr Trp Gly Thr Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Tyr Pro Tyr Tyr Arg Gln Asn Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids

(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Tyr Pro Tyr Tyr Arg Gln Ser Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Tyr Pro Tyr Tyr Arg Asn Thr Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Tyr Pro Tyr Tyr Lys Asn Thr Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Tyr Pro Tyr Tyr Ile Glu Arg Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Tyr Pro Tyr Tyr Arg Asn Ala Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Tyr Pro Tyr Tyr Thr Thr Arg Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Tyr Pro Tyr Tyr Glu Gly Ser Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Tyr Pro Tyr Tyr Arg Gln Arg Gly His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Tyr Pro Tyr Tyr Thr Gly Arg Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Tyr Pro Tyr Tyr Thr Asn Thr Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Tyr Pro Tyr Tyr Arg Lys Gly Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Tyr Pro Tyr Tyr Thr Gly Ser Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Tyr Pro Tyr Tyr Arg Ser Gly Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Tyr Pro Tyr Tyr Thr Asn Arg Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Tyr Pro Tyr Tyr Arg Asn Ser Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Tyr Pro Tyr Tyr Lys Glu Ser Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Tyr Pro Tyr Tyr Arg Asp Ala Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Tyr Pro Tyr Tyr Arg Gln Lys Gly His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Tyr Pro Tyr Tyr Lys Gly Gly Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Tyr Pro Tyr Tyr Tyr Gly Ala Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Tyr Pro Tyr Tyr Arg Gly Glu Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Tyr Pro Tyr Tyr Arg Ser Thr Ser His Trp Tyr Phe Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Gly Tyr Asp Phe Thr His Tyr Gly Met Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Gly Tyr Glu Phe Gln His Tyr Gly Met Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Gly Tyr Glu Phe Thr His Tyr Gly Met Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Gly Tyr Asp Phe Gly His Tyr Gly Met Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Gly Tyr Asp Phe Ser His Tyr Gly Met Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Gly Tyr Glu Phe Ser His Tyr Gly Met Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Phe Ser Val Asp Val Ser Lys Ser Thr Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Phe Ser Leu Asp Lys Ser Lys Ser Thr Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Phe Ser Leu Asp Val Trp Lys Ser Thr Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Phe Ser Ile Asp Lys Ser Lys Ser Thr Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GCAAAGTACC CGTACTATTA TGGGACGAGC CACTGGTATT TC 42

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GTCACCATCA CCTGCAGCGC AAGTCAGGAT ATTAGCAACT ATTTAAAC 48

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

CCGTACTATT ATGGGAGCAG CCACTGGTAT TTC 33

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6072 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC 50
TCATTGCTGA GTTGTATTAT AAGCTTTGGA GATTATCGTC ACTGCAATGC 100
TTCGCAATAT GGCGCAAAAT GACCAACAGC GGTGATTGA TCAGGTAGAG 150
GGGGCGCTGT ACGAGGTAAA GCCCGATGCC AGCATTCCTG ACGACGATAC 200
GGAGCTGCTG CGCGATTACG TAAAGAAGTT ATTGAAGCAT CCTCGTCAGT 250
AAAAAGTTAA TCTTTTCAAC AGCTGTCATA AAGTTGTCAC GGCCGAGACT 300
TATAGTCGCT TTGTTTTTAT TTTTAAATGT ATTTGTAACT AGAATTCGAG 350
CTCGGTACCC GGGGATCCTC TAGAGGTTGA GGTGATTTTA TGAAAAAGAA 400
TATCGCATTT CTTCTTGCACT CTATGTTCTG TTTTCTATT GCTACAAACG 450
CGTACGCTGA TATCCAGTTG ACCCAGTCCC CGAGCTCCCT GTCCGCCTCT 500
GTGGGCGATA GGGTCACCAT CACCTGCAGC GCAAGTCAGG ATATTAGCAA 550
CTATTTAAAC TGGTATCAAC AGAAACCAGG AAAAGCTCCG AAACACTGA 600
TTTACTTCAC CTCCTCTCTC CACTCTGGAG TCCCTTCTCG CTTCTCTGGA 650
TCCGGTTCTG GGACGGATTA CACTCTGACC ATCAGCAGTC TGCAGCCAGA 700
AGACTTCGCA ACTTATTACT GTCAACAGTA TAGCACCGTG CCGTGGACGT 750
TTGGACAGGG TACCAAGGTG GAGATCAAAC GAACTGTGGC TGCACCATCT 800
GTCTTCATCT TCCCGCCATC TGATGAGCAG TTGAAATCTG GAACTGCTTC 850
TGTTGTGTGC CTGCTGAATA ACTTCTATCC CAGAGAGGCC AAAGTACAGT 900
GGAAGGTGGA TAACGCCCTC CAATCGGGTA ACTCCCAGGA GAGTGTACACA 950
GAGCAGGACA GCAAGGACAG CACCTACAGC CTCAGCAGCA CCCTGACGCT 1000
GAGCAAAGCA GACTACGAGA AACACAAAGT CTACGCCTGC GAAGTCACCC 1050
ATCAGGGCCT GAGCTCGCCC GTCACAAAGA GCTTCAACAG GGGAGAGTGT 1100
TAAGCTGATC CTCTACGCCG GACGCATCGT GGCCCTAGTA CGCAACTAGT 1150
CGTAAAAAGG GTATCTAGAG GTTGAGGTGA TTTTATGAAA AAGAATATCG 1200
CATTTCTTCT TGCATCTATG TTCGTTTTTT CTATTGCTAC AAACGCGTAC 1250
GCTGAGGTTC AGCTGGTGGA GTCTGGCGGT GGCCTGGTGC AGCCAGGGGG 1300
CTCACTCCGT TTGTCCTGTG CAGCTTCTGG CTATACCTTC ACCAACTATG 1350
GTATGAACTG GATCCGTCAG GCCCCGGGTA AGGGCCTGGA ATGGGTTGGA 1400
TGGATTAACA CCTATACCGG TGAACCGACC TATGCTGCGG ATTTCAAACG 1450

TCGTTTTACT ATATCTGCAG ACACCTCCAG CAACACAGTT TACCTGCAGA 1500
 TGAACAGCCT GCGCGCTGAG GACACTGCCG TCTATTACTG TGCAAAGTAC 1550
 CCGCACTATT ATGGGAGCAG CCACTGGTAT TTCGACGTCT GGGGTCAAGG 1600
 AACCTGGTC ACCGTCTCCT CGGCCTCCAC CAAGGGCCCA TCGGTCTTCC 1650
 CCCTGGCACC CTCCTCCAAG AGCACCTCTG GGGGCACAGC GGCCCTGGGC 1700
 TGCCTGGTCA AGGACTACTT CCCCGAACCG GTGACGGTGT CGTGGAAGTC 1750
 AGGCGCCCTG ACCAGCGGCG TGCACACCTT CCCGGCTGTC CTACAGTCCT 1800
 CAGGACTCTA CTCCTCAGC AGCGTGGTGA CCGTGCCCTC CAGCAGCTTG 1850
 GGCACCCAGA CCTACATCTG CAACGTGAAT CACAAGCCCA GCAACACCAA 1900
 GGTGACAAG AAAGTTGAGC CCAAATCTTG TGACAAAAC CACCTCTAGA 1950
 GTGGCGGTGG CTCTGGTTCC GGTGATTTTG ATTATGAAA GATGGCAAAC 2000
 GCTAATAAGG GGGCTATGAC CGAAAATGCC GATGAAAACG CGCTACAGTC 2050
 TGACGCTAAA GGCAAAGTTG ATTCTGTCGC TACTGATTAC GGTGCTGCTA 2100
 TCGATGGTTT CATTGGTGAC GTTCCGGCC TTGCTAATGG TAATGGTGCT 2150
 ACTGGTGATT TTGCTGGCTC TAATCCCAA ATGGCTCAAG TCGGTGACGG 2200
 TGATAATTCA CCTTTAATGA ATAATTTCCG TCAATATTTA CCTTCCCTCC 2250
 CTCAATCGGT TGAATGTCGC CCTTTGTCT TTAGCGCTGG TAAACCATAT 2300
 GAATTTTCTA TTGATTGTGA CAAAATAAAC TTATTCCGTG GTGTCTTTGC 2350
 GTTCTTTTA TATGTTGCCA CCTTTATGTA TGTATTTTCT ACGTTTGCTA 2400
 ACATACTGCG TAATAAGGAG TCTTAATCAT GCCAGTTCTT TTGGCTAGCG 2450
 CCGCCCTATA CCTTGTCTGC CTCCCCGCGT TGCCTCGCGG TGCATGGAGC 2500
 CGGGCCACCT CGACCTGAAT GGAAGCCGGC GGCACCTCGC TAACGGATTC 2550
 ACCACTCCAA GAATTGGAGC CAATCAATTC TTGCGGAGAA CTGTGAATGC 2600
 GCAAACCAAC CCTTGGCAGA ACATATCCAT CGCGTCCGCC ATCTCCAGCA 2650
 GCCGCACGCG GCGCATCTCG GGCAGCGTTG GGTCTTGGCC ACGGGTGCGC 2700
 ATGATCGTGC TCCTGTCGTT GAGGACCCGG CTAGGCTGGC GGGGTTGCCT 2750
 TACTGGTTAG CAGAAATGAAT CACCGATACG CGAGCGAACG TGAAGCGACT 2800
 GCTGCTGCAA AACGTCTGCG ACCTGAGCAA CAACATGAAT GGTCTTCGGT 2850
 TTCCGTGTTT CGTAAAGTCT GGAAACGCGG AAGTCAGCGC CCTGCACCAT 2900
 TATGTTCCGG ATCTGCATCG CAGGATGCTG CTGGCTACCC TGTGGAACAC 2950

CTACATCTGT ATTAACGAAG CGCTGGCATT GACCCTGAGT GATTTTTCTC 3000
 TGGTCCCGCC GCATCCATAC CGCCAGTTGT TTACCCTCAC AACGTTCCAG 3050
 TAACCGGGCA TGTTCATCAT CAGTAACCCG TATCGTGAGC ATCCTCTCTC 3100
 GTTTCATCGG TATCATTACC CCCATGAACA GAAATTCCCC CTTACACGGA 3150
 GGCATCAAGT GACCAAACAG GAAAAAACCG CCCTTAACAT GGCCCGCTTT 3200
 ATCAGAAGCC AGACATTAAC GCTTCTGGAG AAACCTCAACG AGCTGGACGC 3250
 GGATGAACAG GCAGACATCT GTGAATCGCT TCACGACCAC GCTGATGAGC 3300
 TTTACCGCAG GATCCGAAA TTGTAAACGT TAATATTTTG TTAATAATTCG 3350
 CGTTAAATTT TTGTAAATC AGCTCATTTT TTAACCAATA GGCCGAAATC 3400
 GGCAAAATCC CTTATAAATC AAAAGAATAG ACCGAGATAG GGTGAGTGT 3450
 TGTTCAGTT TGAACAAGA GTCCACTATT AAAGAACGTG GACTCCAACG 3500
 TCAAAGGGCG AAAAACCGTC TATCAGGGCT ATGGCCCACT ACGTGAACCA 3550
 TCACCCTAAT CAAGTTTTTT GGGGTCGAGG TGCCGTAAAG CACTAAATCG 3600
 GAACCCTAAA GGGAGCCCC GATTTAGAGC TTGACGGGGA AAGCCGGCGA 3650
 ACGTGGCGAG AAAGGAAGGG AAGAAAGCGA AAGGAGCGGG CGCTAGGGCG 3700
 CTGGCAAGTG TAGCGGTCAC GCTGCGCGTA ACCACCACAC CCGCCGCGCT 3750
 TAATGCGCCG CTACAGGGCG CGTCCGATC CTGCCTCGCG CGTTTCGGTG 3800
 ATGACGGTGA AAACCTCTGA CACATGCAGC TCCCGGAGAC GGTCACAGCT 3850
 TGTCTGTAAG CGGATGCCGG GAGCAGACAA GCCCGTCAGG GCGCGTCAGC 3900
 GGGTGTGGC GGGTGTGGG GCGCAGCCAT GACCCAGTCA CGTAGCGATA 3950
 GCGGAGTGTA TACTGGCTTA ACTATGCGGC ATCAGAGCAG ATTGTACTGA 4000
 GAGTGCACCA TATGCGGTGT GAAATACCGC ACAGATGCGT AAGGAGAAAA 4050
 TACCGCATCA GCGGCTCTTC CGCTTCCTCG CTCACTGACT CGCTGCGCTC 4100
 GGTCGTTCGG CTGCGGCGAG CGGTATCAGC TCACTCAAAG GCGGTAATAC 4150
 GGTTATCCAC AGAATCAGGG GATAACGCAG GAAAGAACAT GTGAGCAAAA 4200
 GGCCAGCAAA AGGCCAGGAA CCGTAAAAAG GCCGCGTTGC TGGCGTTTTT 4250
 CCATAGGCTC CGCCCCCTG ACGAGCATCA CAAAAATCGA CGCTCAAGTC 4300
 AGAGGTGGCG AAACCCGACA GGAATAAAA GATACCAGGC GTTTCCCCCT 4350
 GGAAGCTCCC TCGTGCGCTC TCCTGTTCCG ACCCTGCCGC TTACCGGATA 4400
 CCTGTCCGCC TTTCTCCCTT CGGGAAGCGT GCGGCTTTCT CATAGCTCAC 4450
 GCTGTAGGTA TCTCAGTTCG GTGTAGGTCG TTCGCTCAA GCTGGGCTGT 4500

GTGCACGAAC CCCCCGTTCA GCCCGACCGC TGCGCCTTAT CCGGTA ACTA 4550
 TCGTCTTGAG TCCAACCCGG TAAGACACGA CTTATCGCCA CTGGCAGCAG 4600
 CCACTGGTAA CAGGATTAGC AGAGCGAGGT ATGTAGGCGG TGCTACAGAG 4650
 TTCTTGAAGT GGTGGCCTAA CTACGGCTAC ACTAGAAGGA CAGTATTTGG 4700
 TATCTGCGCT CTGCTGAAGC CAGTTACCTT CGGAAAAAGA GTTGGTAGCT 4750
 CTTGATCCGG CAAACAAACC ACCGCTGGTA GCGGTGGTTT TTTTGTTC 4800
 AAGCAGCAGA TTACGCGCAG AAAAAAGGA TCTCAAGAAG ATCCTTTGAT 4850
 CTTTCTACG GGGTCTGACG CTCAGTGGAA CGAAACTCA CGTTAAGGGA 4900
 TTTTGGTCAT GAGATTATCA AAAAGGATCT TCACCTAGAT CCTTTTAAAT 4950
 TAAAAATGAA GTTTTAAATC AATCTAAAGT ATATATGAGT AAAGTTGGTC 5000
 TGACAGTTAC CAATGCTTAA TCAGTGAGGC ACCTATCTCA GCGATCTGTC 5050
 TATTTTCGTC ATCCATAGTT GCCTGACTCC CCGTCGTGTA GATAACTACG 5100
 ATACGGGAGG GCTTACCATC TGGCCCCAGT GCTGCAATGA TACCGCGAGA 5150
 CCCACGCTCA CCGGCTCCAG ATTTATCAGC AATAAACCAG CCAGCCGGAA 5200
 GGGCCGAGCG CAGAAGTGGT CCTGCAACTT TATCCGCCTC CATCCAGTCT 5250
 ATTAATTGTT GCCGGGAAGC TAGAGTAAGT AGTTCGCCAG TTAATAGTTT 5300
 GCGCAACGTT GTTGCCATTG CTGCAGGCAT CGTGGTGTCA CGCTCGTCGT 5350
 TTGGTATGGC TTCATTACG TCCGGTTCCC AACGATCAAG GCGAGTTACA 5400
 TGATCCCCCA TGTTGTGCAA AAAAGCGGTT AGCTCCTTCG GTCCTCCGAT 5450
 CGTTGTCAGA AGTAAGTTGG CCGCAGTGTT ATCACTCATG GTTATGGCAG 5500
 CACTGCATAA TTCTCTTACT GTCATGCCAT CCGTAAGATG CTTTTCTGTG 5550
 ACTGGTGAGT ACTCAACCAA GTCATTCTGA GAATAGTGTA TGCGGCGACC 5600
 GAGTTGCTCT TGGCCGGCGT CAACACGGGA TAATACCGCG CCACATAGCA 5650
 GAACTTTAAA AGTGCTCATC ATTGGAAAAC GTTCTTCGGG GCGAAAACTC 5700
 TCAAGGATCT TACCGCTGTT GAGATCCAGT TCGATGTAAC CCACTCGTGC 5750
 ACCCAACTGA TCTTCAGCAT CTTTTACTTT CACCAGCGTT TCTGGGTGAG 5800
 CAAAAACAGG AAGGCAAAAT GCCGCAAAAA AGGGAATAAG GGCGACACGG 5850
 AAATGTTGAA TACTCATACT CTTCTTTTTT CAATATTATT GAAGCATTTA 5900
 TCAGGGTTAT TGTCTCATGA GCGGATACAT ATTTGAATGT ATTTAGAAAA 5950
 ATAAACAAAT AGGGGTTCG CGCACATTC CCCGAAAAGT GCCACCTGAC 6000

GTCTAAGAAA CCATTATTAT CATGACATTA ACCTATAAAA ATAGGCGTAT 6050
CACGAGGCCC TTTCGTCTTC AA 6072

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 amino acids
 - (B) TYPE: PRT
 - (D) TOPOLOGY:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	1	5	10	15
Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Asp	Ile	Gln	Leu	Thr	Gln	Ser	20	25	30	
Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	35	40	45	
Cys	Ser	Ala	Ser	Gln	Asp	Ile	Ser	Asn	Tyr	Leu	Asn	Trp	Tyr	Gln	50	55	60	
Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Phe	Thr	Ser	65	70	75	
Ser	Leu	His	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	80	85	90	
Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	95	100	105	
Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Ser	Thr	Val	Pro	Trp	Thr	110	115	120	
Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	125	130	135	
Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	140	145	150	
Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	155	160	165	
Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	170	175	180	
Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	185	190	195	
Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	200	205	210	
Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	215	220	225	
Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys	230	235					

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	
1				5					10					15	
Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser	Gln	Asp	Ile	Ser	
				20					25					30	
Asn	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	
				35					40					45	
Leu	Leu	Ile	Tyr	Phe	Thr	Ser	Ser	Leu	His	Ser	Gly	Val	Pro	Ser	
				50					55					60	
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	
				65					70					75	
Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	
				80					85					90	
Tyr	Ser	Thr	Val	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	
				95					100					105	
Ile	Lys	Arg	Thr	Val											
				110											

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	
1				5					10					15	
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	
				20					25					30	
Asn	Tyr	Gly	Met	Asn	Trp	Ile	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
				35					40					45	
Glu	Trp	Val	Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Gly	Glu	Pro	Thr	Tyr	
				50					55					60	
Ala	Ala	Asp	Phe	Lys	Arg	Arg	Phe	Thr	Ile	Ser	Ala	Asp	Thr	Ser	•
				65					70					75	
Ser	Asn	Thr	Val	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	
				80					85					90	

Thr Ala Val Tyr Tyr Cys Ala Lys Tyr Pro His Tyr Tyr Gly Ser
95 100 105

Ser His Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu
110 115

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1 5 10 15

Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile Ser
20 25 30

Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
35 40 45

Val Leu Ile Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile
65 70 75

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
80 85 90

Tyr Ser Thr Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
95 100 105

Ile Lys Arg Thr Val
110

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr
20 25 30

Asn Tyr Gly Met Asn Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45

Glu Trp Val Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr
50 55 60

Ala	Ala	Asp	Phe	Lys	Arg	Arg	Phe	Thr	Phe	Ser	Ala	Asp	Thr	Ser
				65					70					75
Ser	Asn	Thr	Val	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp
				80					85					90
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Tyr	Pro	His	Tyr	Tyr	Gly	Ser
				95					100					105
Ser	His	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Leu		
				110					115					

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val
1				5					10					15
Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser	Gln	Asp	Ile	Ser
				20					25					30
Asn	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys
				35					40					45
Val	Leu	Ile	Tyr	Phe	Thr	Ser	Ser	Leu	His	Ser	Gly	Val	Pro	Ser
				50					55					60
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile
				65					70					75
Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln
				80					85					90
Tyr	Ser	Thr	Val	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu
				95					100					105
Ile	Lys	Arg	Thr	Val										
				110										

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly
1				5					10					15
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Thr	Phe	Thr
				20					25					30

Asn	Tyr	Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
				35					40					45
Glu	Trp	Val	Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Gly	Glu	Pro	Thr	Tyr
				50					55					60
Ala	Ala	Asp	Phe	Lys	Arg	Arg	Phe	Thr	Phe	Ser	Leu	Asp	Thr	Ser
				65					70					75
Lys	Ser	Thr	Ala	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp
				80					85					90
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Tyr	Pro	His	Tyr	Tyr	Gly	Ser
				95					100					105
Ser	His	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Leu		
				110					115					

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val
1				5					10					15
Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Asn	Glu	Gln	Leu	Ser
				20					25					30
Asn	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys
				35					40					45
Val	Leu	Ile	Tyr	Phe	Thr	Ser	Ser	Leu	His	Ser	Gly	Val	Pro	Ser
				50					55					60
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile
				65					70					75
Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln
				80					85					90
Tyr	Ser	Thr	Val	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu
				95					100					105
Ile	Lys	Arg	Thr	Val										
				110										

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	1	5	10	15
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	20	25	30	
Asn	Tyr	Gly	Ile	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	35	40	45	
Glu	Trp	Val	Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Gly	Glu	Pro	Thr	Tyr	50	55	60	
Ala	Ala	Asp	Phe	Lys	Arg	Arg	Phe	Thr	Phe	Ser	Leu	Asp	Thr	Ser	65	70	75	
Lys	Ser	Thr	Ala	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	80	85	90	
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Tyr	Pro	His	Tyr	Tyr	Gly	Ser	95	100	105	
Ser	His	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Leu	110	115				

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	1	5	10	15
Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Asn	Glu	Gln	Leu	Ser	20	25	30	
Asn	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	35	40	45	
Val	Leu	Ile	Tyr	Phe	Thr	Ser	Ser	Leu	His	Ser	Gly	Val	Pro	Ser	50	55	60	
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	65	70	75	
Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	80	85	90	
Tyr	Ser	Thr	Val	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	95	100	105	
Ile	Lys	Arg	Thr	Val	110													

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 amino acids

(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	
1				5					10					15	
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Asp	Phe	Thr	
				20					25					30	
His	Tyr	Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
				35					40					45	
Glu	Trp	Val	Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Gly	Glu	Pro	Thr	Tyr	
				50					55					60	
Ala	Ala	Asp	Phe	Lys	Arg	Arg	Phe	Thr	Phe	Ser	Leu	Asp	Thr	Ser	
				65					70					75	
Lys	Ser	Thr	Ala	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	
				80					85					90	
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Tyr	Pro	His	Tyr	Tyr	Gly	Ser	
				95					100					105	
Ser	His	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Leu			
				110					115						

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	
1				5					10					15	
Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Asn	Glu	Gln	Leu	Ser	
				20					25					30	
Asn	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	
				35					40					45	
Val	Leu	Ile	Tyr	Phe	Thr	Ser	Ser	Leu	His	Ser	Gly	Val	Pro	Ser	
				50					55					60	
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	
				65					70					75	
Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	
				80					85					90	
Tyr	Ser	Thr	Val	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	
				95					100					105	
Ile	Lys	Arg	Thr	Val											
				110											

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	
1				5					10					15	
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	
				20					25					30	
Asn	Tyr	Gly	Ile	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
				35					40					45	
Glu	Trp	Val	Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Gly	Glu	Pro	Thr	Tyr	
				50					55					60	
Ala	Ala	Asp	Phe	Lys	Arg	Arg	Phe	Thr	Phe	Ser	Leu	Asp	Thr	Ser	
				65					70					75	
Lys	Ser	Thr	Ala	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	
				80					85					90	
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Tyr	Pro	Tyr	Tyr	Tyr	Gly	Thr	
				95					100					105	
Ser	His	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Leu			
				110					115						

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	
1				5					10					15	
Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Asn	Glu	Gln	Leu	Ser	
				20					25					30	
Asn	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	
				35					40					45	
Val	Leu	Ile	Tyr	Phe	Thr	Ser	Ser	Leu	His	Ser	Gly	Val	Pro	Ser	
				50					55					60	
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	
				65					70					75	
Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	
				80					85					90	

Tyr Ser Thr Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
 95 100 105

Ile Lys Arg Thr Val
 110

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
 1 5 10 15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Asp Phe Thr
 20 25 30

His Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 35 40 45

Glu Trp Val Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr
 50 55 60

Ala Ala Asp Phe Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr Ser
 65 70 75

Lys Ser Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
 80 85 90

Thr Ala Val Tyr Tyr Cys Ala Lys Tyr Pro Tyr Tyr Tyr Gly Thr
 95 100 105

Ser His Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu
 110 115

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1 5 10 15

Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile Ser
 20 25 30

Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 35 40 45

Val Leu Ile Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
65 70 75
Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
80 85 90
Tyr Ser Thr Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
95 100 105
Ile Lys Arg Thr Val
110

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15
Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Asp Phe Thr
20 25 30
His Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45
Glu Trp Val Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr
50 55 60
Ala Ala Asp Phe Lys Arg Arg Phe Thr Phe Ser Leu Asp Thr Ser
65 70 75
Lys Ser Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
80 85 90
Thr Ala Val Tyr Tyr Cys Ala Lys Tyr Pro Tyr Tyr Tyr Gly Thr
95 100 105
Ser His Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu
110 115

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Where the X at position 3 represents either Aspartic acid, Threonine or Glutamic acid

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

(B) LOCATION: 4
 (C) IDENTIFICATION METHOD:
 (D) OTHER INFORMATION: Where the X at position 4 represents either Phenylalanine, Tryptophan or Tyrosine

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 5
 (C) IDENTIFICATION METHOD:
 (D) OTHER INFORMATION: Where the X at position 5 represents either Threonine, Glutamine, Glycine or Serine

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 6
 (C) IDENTIFICATION METHOD:
 (D) OTHER INFORMATION: Where the X at position 6 is either Histidine or Asparagine

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 9
 (C) IDENTIFICATION METHOD:
 (D) OTHER INFORMATION: Where the X at position 9 represents either Methionine or Isoleucine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Gly	Tyr	Xaa	Xaa	Xaa	Xaa	Tyr	Gly	Xaa	Asn
1				5					10

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 5
 (C) IDENTIFICATION METHOD:
 (D) OTHER INFORMATION: Where the X at position 5 represents either Tyrosine or Tryptophan

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Trp	Ile	Asn	Thr	Xaa	Thr	Gly	Glu	Pro	Thr	Tyr	Ala	Ala	Asp	Phe
1				5					10					15

Lys Arg

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Where the X at position 3 represents either
Histidine or Tyrosine

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Where the X at position 5 represents either
Tyrosine, Arginine, Lysine, Isoleucine, Threonine, Glutamic acid or
Tryptophan

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 6
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Where the X at position 6 represents either
glycine, Arginine, Alanine, Aspartic acid, Glutamine, Glutamic acid,
Threonine, Leucine aor Serine

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 7
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Where the X at position 7 represents either
Serine, Threonine, Lysine, Glutamine, Asparagine, Arginine, Alanine, Glutamic
acid or Glycine

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 8
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Where the X at position 8 represents either
Serine or Glycine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Tyr Pro Xaa Tyr Xaa Xaa Xaa Xaa His Trp Tyr Phe Asp Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Where the X at position 1 represents either
Phenylalanine, Isoleucine, Valine, Leucine or Alanine

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION: Where the X at position 3 represents either Alanine, Leucine, Valine or Isoleucine

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Where the X at position 5 represents either Threonine, Valine or Lysine

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Where the X at position 6 represents either Serine or Tryptophan

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Where the X at position 7 represents either Serine or Lysine

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Where the X at position 8 represents either Asparagine or Serine

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Where the X at position 10 represents either Valine, Alanine, Leucine or Isoleucine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Xaa	Ser	Xaa	Asp	Xaa	Xaa	Xaa	Xaa	Thr	Xaa
1				5					10

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Where the X at position 1 represents either Arginine or Serine

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION: Where the X at position 3 represents either Serine or Asparagine

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 4

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION: Where the X at position 4 represents either Glutamine or Glutamic acid

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 5

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION: Where the X at position 5 represents either Glutamine or Aspartic acid

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 6

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION: Where the X at position 6 represents either Isoleucine or Leucine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Xaa	Ala	Xaa	Xaa	Xaa	Xaa	Ser	Asn	Tyr	Leu	Asn
1				5					10	

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Phe	Thr	Ser	Ser	Leu	His	Ser
1				5		

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 5

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION: Where the X at position 5 represents either Threonine, Alanine or Asparagine

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 6

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION: Where the X at position 6 represents either Valine or Threonine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Gln Gln Tyr Ser Xaa Xaa Pro Trp Thr
1 5

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 4

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION: Where the X at position 4 represents either Methionine or Leucine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Asp Ile Gln Xaa Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1 5 10 15

Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Asp Ile Ser
20 25 30

Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
35 40 45

Val Leu Ile Tyr Phe Thr Ser Ser Leu His Ser Gly Val Pro Ser
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
65 70 75

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
80 85 90

Tyr Ser Thr Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
95 100 105

Ile Lys Arg

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 28

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION: Where the X at position 28 represents either Threonine or Aspartic acid

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 31
 (C) IDENTIFICATION METHOD:
 (D) OTHER INFORMATION: Where the X at position 31 represents either Asparagine or Histidine

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 101
 (C) IDENTIFICATION METHOD:
 (D) OTHER INFORMATION: Where the X at position 101 represents either Tyrosine or Histidine

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 105
 (C) IDENTIFICATION METHOD:
 (D) OTHER INFORMATION: Where the X at position 105 represents either Serine or Threonine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	1	5	10	15
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Xaa	Phe	Thr	20	25	30	
Xaa	Tyr	Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	35	40	45	
Glu	Trp	Val	Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Gly	Glu	Pro	Thr	Tyr	50	55	60	
Ala	Ala	Asp	Phe	Lys	Arg	Arg	Phe	Thr	Phe	Ser	Leu	Asp	Thr	Ser	65	70	75	
Lys	Ser	Thr	Ala	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	80	85	90	
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Tyr	Pro	Xaa	Tyr	Tyr	Gly	Xaa	95	100	105	
Ser	His	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	110	115	120	
Val	Ser	Ser																

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Gly	Tyr	Asp	Phe	Thr	His	Tyr	Gly	Met	Asn	1	5	10
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(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Tyr Pro Tyr Tyr Tyr Gly Thr Ser His Trp Tyr Phe Asp Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Where the X at position 3 represents either Threonine or Aspartic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Gly Tyr Xaa Phe Thr Xaa Tyr Gly Met Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Where the X at position 3 represents either Tyrosine or Histidine

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION: Where the X at position 7 represents either Serine or Threonine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Tyr Pro Xaa Tyr Tyr Gly Xaa Ser His Trp Tyr Phe Asp Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids

(B) TYPE: PRT
(D) TOPOLOGY:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	1	5	10	15
Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Glu	Val	Gln	Leu	Val	Glu	Ser	20	25	30	
Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	35	40	45	
Ala	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr	Gly	Met	Asn	Trp	Ile	50	55	60	
Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Gly	Trp	Ile	Asn	65	70	75	
Thr	Tyr	Thr	Gly	Glu	Pro	Thr	Tyr	Ala	Ala	Asp	Phe	Lys	Arg	Arg	80	85	90	
Phe	Thr	Ile	Ser	Ala	Asp	Thr	Ser	Ser	Asn	Thr	Val	Tyr	Leu	Gln	95	100	105	
Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	110	115	120	
Lys	Tyr	Pro	His	Tyr	Tyr	Gly	Ser	Ser	His	Trp	Tyr	Phe	Asp	Val	125	130	135	
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	140	145	150	
Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	155	160	165	
Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	170	175	180	
Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	185	190	195	
Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	200	205	210	
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	215	220	225	
Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	230	235	240	
Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Leu		245	250		

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 158 amino acids
 (B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Ser	Gly	Gly	Gly	Ser	Gly	Ser	Gly	Asp	Phe	Asp	Tyr	Glu	Lys	Met
1				5				10						15
Ala	Asn	Ala	Asn	Lys	Gly	Ala	Met	Thr	Glu	Asn	Ala	Asp	Glu	Asn
				20					25					30
Ala	Leu	Gln	Ser	Asp	Ala	Lys	Gly	Lys	Leu	Asp	Ser	Val	Ala	Thr
				35					40					45
Asp	Tyr	Gly	Ala	Ala	Ile	Asp	Gly	Phe	Ile	Gly	Asp	Val	Ser	Gly
				50					55					60
Leu	Ala	Asn	Gly	Asn	Gly	Ala	Thr	Gly	Asp	Phe	Ala	Gly	Ser	Asn
				65					70					75
Ser	Gln	Met	Ala	Gln	Val	Gly	Asp	Gly	Asp	Asn	Ser	Pro	Leu	Met
				80					85					90
Asn	Asn	Phe	Arg	Gln	Tyr	Leu	Pro	Ser	Leu	Pro	Gln	Ser	Val	Glu
				95					100					105
Cys	Arg	Pro	Phe	Val	Phe	Ser	Ala	Gly	Lys	Pro	Tyr	Glu	Phe	Ser
				110					115					120
Ile	Asp	Cys	Asp	Lys	Ile	Asn	Leu	Phe	Arg	Gly	Val	Phe	Ala	Phe
				125					130					135
Leu	Leu	Tyr	Val	Ala	Thr	Phe	Met	Tyr	Val	Phe	Ser	Thr	Phe	Ala
				140					145					150
Asn	Ile	Leu	Arg	Asn	Lys	Glu	Ser							
				155										